



SEQUENCE LISTING

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<120> CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
CYCLASE

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<150> 08/886,440

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<170> PatentIn Ver. 2.0

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			500					505					510		
Asp	Val	Asn	Leu	Ala	Asn	Leu	Met	Glu	Gln	Leu	Gly	Val	Ala	Gly	Lys
		515					520					525			
Val	His	Ile	Ser	Glu	Ala	Thr	Ala	Lys	Tyr	Leu	Asp	Asp	Arg	Tyr	Glu

530	535	540														
Met	Glu	Asp	Gly	Lys	Val	Ile	Glu	Arg	Leu	Gly	Gln	Ser	Val	Val	Ala	
545					550					555					560	
Asp	Gln	Leu	Lys	Gly	Leu	Lys	Thr	Tyr	Leu	Ile	Ser	Gly	Gln	Arg	Ala	
			565						570					575		
Lys	Glu	Ser	Arg	Cys	Ser	Cys	Ala	Glu	Ala	Leu	Leu	Ser	Gly	Phe	Glu	
			580					585					590			
Val	Ile	Asp	Gly	Ser	Gln	Val	Ser	Ser	Gly	Pro	Arg	Gly	Gln	Gly	Thr	
		595					600					605				
Ala	Ser	Ser	Gly	Asn	Val	Ser	Asp	Leu	Ala	Gln	Thr	Val	Lys	Thr	Phe	
	610					615					620					
Asp	Asn	Leu	Lys	Thr	Cys	Pro	Ser	Cys	Gly	Ile	Thr	Phe	Ala	Pro	Lys	
625					630					635					640	
Ser	Glu	Ala	Gly	Ala	Glu	Gly	Gly	Ala	Pro	Gln	Asn	Gly	Cys	Gln	Asp	
			645					650						655		
Glu	His	Lys	Asn	Ser	Thr	Lys	Ala	Ser	Gly	Gly	Pro	Asn	Pro	Lys	Thr	
		660						665					670			
Gln	Asn	Gly	Leu	Leu	Ser	Pro	Pro	Gln	Glu	Glu	Lys	Leu	Thr	Asn	Ser	
	675						680						685			
Gln	Thr	Ser	Leu	Cys	Glu	Ile	Leu	Gln	Glu	Lys	Gly	Arg	Trp	Ala	Gly	
	690					695					700					
Val	Ser	Leu	Asp	Gln	Ser	Ala	Leu	Leu	Pro	Leu	Arg	Phe	Lys	Asn	Ile	
705					710					715					720	
Arg	Glu	Lys	Thr	Asp	Ala	His	Phe	Val	Asp	Val	Ile	Lys	Glu	Asp	Ser	
			725						730					735		
Leu	Met	Lys	Asp	Tyr	Phe	Phe	Lys	Pro	Pro	Ile	Asn	Gln	Phe	Ser	Leu	
		740						745					750			
Asn	Phe	Leu	Asp	Gln	Glu	Leu	Glu	Arg	Ser	Tyr	Arg	Thr	Ser	Tyr	Gln	
	755						760					765				
Glu	Glu	Val	Ile	Lys	Asn	Ser	Pro	Val	Lys	Thr	Phe	Ala	Ser	Pro	Thr	
	770					775					780					
Phe	Ser	Ser	Leu	Leu	Asp	Val	Phe	Leu	Ser	Thr	Thr	Val	Phe	Leu	Thr	
785					790					795					800	
Leu	Ser	Thr	Thr	Cys	Phe	Leu	Lys	Tyr	Glu	Ala	Ala	Thr	Val	Pro	Pro	
			805						810					815		
Pro	Pro	Ala	Ala	Leu	Ala	Val	Phe	Ser	Ala	Ala	Leu	Leu	Leu	Glu	Val	
		820						825					830			
Leu	Ser	Leu	Ala	Val	Ser	Ile	Arg	Met	Val	Phe	Phe	Leu	Glu	Asp	Val	

835	840	845
Met Ala Cys Thr Lys Arg Leu Leu Glu Trp Ile Ala Gly Trp Leu Pro 850 855 860		
Arg His Cys Ile Gly Ala Ile Leu Val Ser Leu Pro Ala Leu Ala Val 865 870 875 880		
Tyr Ser His Val Thr Ser Glu Tyr Glu Thr Asn Ile His Phe Pro Val 885 890 895		
Phe Thr Gly Ser Ala Ala Leu Ile Ala Val Val His Tyr Cys Asn Phe 900 905 910		
Cys Gln Leu Ser Ser Trp Met Arg Ser Ser Leu Ala Thr Val Val Gly 915 920 925		
Ala Gly Pro Leu Leu Leu Leu Tyr Val Ser Leu Cys Pro Asp Ser Ser 930 935 940		
Val Leu Thr Ser Pro Leu Asp Ala Val Gln Asn Phe Ser Ser Glu Arg 945 950 955 960		
Asn Pro Cys Asn Ser Ser Val Pro Arg Asp Leu Arg Arg Pro Ala Ser 965 970 975		
Leu Ile Gly Gln Glu Val Val Leu Val Phe Phe Leu Leu Leu Leu Leu 980 985 990		
Val Trp Phe Leu Asn Arg Glu Phe Glu Val Ser Tyr Arg Leu His Tyr 995 1000 1005		
His Gly Asp Val Glu Ala Asp Leu His Arg Thr Lys Ile Gln Ser Met 1010 1015 1020		
Arg Asp Gln Ala Asp Trp Leu Leu Arg Asn Ile Ile Pro Tyr His Val 1025 1030 1035 1040		
Ala Glu Gln Leu Lys Val Ser Gln Thr Tyr Ser Lys Asn His Asp Ser 1045 1050 1055		
Gly Gly Val Ile Phe Ala Ser Ile Val Asn Phe Ser Glu Phe Tyr Glu 1060 1065 1070		
Glu Asn Tyr Glu Gly Gly Lys Glu Cys Tyr Arg Val Leu Asn Glu Leu 1075 1080 1085		
Ile Gly Asp Phe Asp Glu Leu Leu Ser Lys Pro Asp Tyr Ser Ser Ile 1090 1095 1100		
Glu Lys Ile Lys Thr Ile Gly Ala Thr Tyr Met Ala Ala Ser Gly Leu 1105 1110 1115 1120		
Asn Thr Ala Gln Ala Gln Asp Gly Ser His Pro Gln Glu His Leu Gln 1125 1130 1135		
Ile Leu Phe Glu Phe Ala Lys Glu Met Met Arg Val Val Asp Asp Phe		

1140					1145					1150						
Asn	Asn	Asn	Met	Leu	Trp	Phe	Asn	Phe	Lys	Leu	Arg	Val	Gly	Phe	Asn	
1155					1160					1165						
His	Gly	Pro	Leu	Thr	Ala	Gly	Val	Ile	Gly	Thr	Thr	Lys	Leu	Leu	Tyr	
1170					1175					1180						
Asp	Ile	Trp	Gly	Asp	Thr	Val	Asn	Ile	Ala	Ser	Arg	Met	Asp	Thr	Thr	
1185					1190					1195					1200	
Gly	Val	Glu	Cys	Arg	Ile	Gln	Val	Ser	Glu	Glu	Ser	Tyr	Arg	Val	Leu	
1205					1210					1215						
Ser	Lys	Met	Gly	Tyr	Asp	Phe	Asp	Tyr	Arg	Gly	Thr	Val	Asn	Val	Lys	
1220					1225					1230						
Gly	Lys	Gly	Gln	Met	Lys	Thr	Tyr	Leu	Tyr	Pro	Lys	Cys	Thr	Asp	His	
1235					1240					1245						
Arg	Val	Ile	Pro	Ala	Pro	Ala	Val	His	Leu	Pro	Arg	His	Pro	Arg	Pro	
1250					1255					1260						
Gly	Gly	Trp	Gln	His	Arg	Thr	Val	Ser	His	Arg	Arg	Asp	Cys	Gln	Pro	
1265					1270					1275					1280	
Gly	Ala	Phe	Cys	Pro	Val	Cys	Gly	Gln	Asp	Ile	Ser	Gly	Phe			
1285					1290											

<210> 3

<211> 1353

<212> PRT

<213> murine type IX adenylyl cyclase

<400> 3

Met	Ala	Ser	Ser	Pro	His	Gln	Gln	Leu	Leu	His	His	His	Ser	Thr	Glu
1				5				10						15	

Val	Ser	Cys	Asp	Ser	Ser	Gly	Asp	Ser	Asn	Ser	Val	Arg	Val	Lys	Ile
			20					25					30		

Asn	Pro	Lys	Gln	Leu	Ser	Ser	Asn	Ile	His	Pro	Lys	His	Cys	Lys	Tyr
			35				40						45		

Ser	Ile	Ser	Ser	Ser	Cys	Ser	Ser	Ser	Gly	Asp	Ser	Gly	Gly	Leu	Pro
	50					55					60				

Arg	Arg	Val	Gly	Gly	Gly	Gly	Arg	Leu	Arg	Arg	Gln	Lys	Lys	Leu	Pro
	65				70						75				80

Gln	Leu	Phe	Glu	Arg	Ala	Ser	Ser	Arg	Trp	Trp	Asp	Pro	Lys	Phe	Asp
				85					90					95	

Ser	Met	Asn	Leu	Glu	Glu	Ala	Cys	Leu	Glu	Arg	Cys	Phe	Pro	Gln	Thr
			100					105					110		

Gln Arg Arg Phe Arg Tyr Ala Leu Phe Tyr Val Gly Phe Ala Cys Leu
 115 120 125
 Leu Trp Ser Ile Tyr Phe Ala Val His Met Lys Ser Lys Val Ile Val
 130 135 140
 Met Val Val Pro Ala Leu Cys Phe Leu Val Val Cys Val Gly Phe Phe
 145 150 155 160
 Leu Phe Thr Phe Thr Lys Leu Tyr Ala Arg His Tyr Ala Trp Thr Ser
 165 170 175
 Leu Ala Leu Thr Leu Leu Val Phe Ala Leu Thr Leu Ala Ala Gln Phe
 180 185 190
 Gln Val Trp Thr Pro Leu Ser Gly Arg Val Asp Ser Ser Asn His Thr
 195 200 205
 Leu Thr Ala Ile Pro Ala Asp Thr Cys Leu Ser Gln Val Gly Ser Phe
 210 215 220
 Ser Ile Cys Ile Glu Val Leu Leu Leu Leu Tyr Thr Val Met Gln Leu
 225 230 235 240
 Pro Leu Tyr Leu Ser Leu Phe Leu Gly Val Val Tyr Ser Val Leu Phe
 245 250 255
 Glu Thr Phe Gly Tyr His Phe Arg Asn Glu Asp Cys Tyr Pro Ser Pro
 260 265 270
 Gly Pro Gly Ala Leu His Trp Glu Leu Leu Ser Arg Ala Leu Leu His
 275 280 285
 Val Cys Ile His Ala Ile Gly Ile His Leu Phe Val Met Ser Gln Val
 290 295 300
 Arg Ser Arg Ser Thr Phe Leu Lys Val Gly Gln Ser Ile Met His Gly
 305 310 315 320
 Lys Asp Leu Glu Val Glu Lys Ala Leu Lys Glu Arg Met Ile His Ser
 325 330 335
 Val Met Pro Arg Ile Ile Ala Asp Asp Leu Met Lys Gln Gly Asp Glu
 340 345 350
 Glu Ser Glu Asn Ser Val Lys Arg His Ala Thr Ser Ser Pro Lys Asn
 355 360 365
 Arg Lys Lys Lys Ser Ser Ile Gln Lys Ala Pro Ile Ala Phe Arg Pro
 370 375 380
 Phe Lys Met Gln Gln Ile Glu Glu Val Ser Ile Leu Phe Ala Asp Ile
 385 390 395 400
 Val Gly Phe Thr Lys Met Ser Ala Asn Lys Ser Ala His Ala Leu Val
 405 410 415

Gly Leu Leu Asn Asp Leu Phe Gly Arg Phe Asp Arg Leu Cys Glu Gln
 420 425 430
 Thr Lys Cys Glu Lys Ile Ser Thr Leu Gly Asp Cys Tyr Tyr Cys Val
 435 440 445
 Ala Gly Cys Pro Glu Pro Arg Ala Asp His Ala Tyr Cys Cys Ile Glu
 450 455 460
 Met Gly Leu Gly Met Ile Lys Ala Ile Glu Gln Phe Cys Gln Glu Lys
 465 470 475 480
 Lys Glu Met Val Asn Met Arg Val Gly Val His Thr Gly Thr Val Leu
 485 490 495
 Cys Gly Ile Leu Gly Met Arg Arg Phe Lys Phe Asp Val Trp Ser Asn
 500 505 510
 Asp Val Asn Leu Ala Asn Leu Met Glu Gln Leu Gly Val Ala Gly Lys
 515 520 525
 Val His Ile Ser Glu Ala Thr Ala Lys Tyr Leu Asp Asp Arg Tyr Glu
 530 535 540
 Met Glu Asp Gly Arg Val Ile Glu Arg Leu Gly Gln Ser Val Val Ala
 545 550 555 560
 Asp Gln Leu Lys Gly Leu Lys Thr Tyr Leu Ile Ser Gly Gln Arg Ala
 565 570 575
 Lys Glu Ser His Cys Ser Cys Ala Glu Ala Leu Leu Ser Gly Phe Glu
 580 585 590
 Val Ile Asp Asp Ser Arg Glu Ser Ser Gly Pro Arg Gly Gln Gly Thr
 595 600 605
 Ala Ser Pro Gly Ser Val Ser Asp Leu Ala Gln Thr Val Lys Thr Phe
 610 615 620
 Asp Asn Leu Lys Thr Cys Pro Ser Cys Gly Ile Thr Phe Ala Pro Lys
 625 630 635 640
 Ser Glu Ala Gly Ala Glu Gly Gly Thr Val Gln Asn Gly Cys Gln Asp
 645 650 655
 Glu Pro Lys Thr Ser Thr Lys Ala Ser Gly Gly Pro Asn Ser Lys Thr
 660 665 670
 Gln Asn Gly Leu Leu Ser Pro Pro Ala Glu Glu Lys Leu Thr Asn Ser
 675 680 685
 Gln Thr Ser Leu Cys Glu Ile Leu Gln Glu Lys Gly Arg Trp Ala Gly
 690 695 700
 Val Ser Leu Asp Gln Ser Ala Leu Leu Pro Leu Arg Phe Lys Asn Ile
 705 710 715 720

Arg Glu Lys Thr Asp Ala His Phe Val Asp Val Ile Lys Glu Asp Ser
 725 730 735
 Leu Met Lys Asp Tyr Phe Phe Lys Pro Pro Ile Asn Gln Phe Ser Leu
 740 745 750
 Asn Phe Leu Asp Gln Glu Leu Glu Arg Ser Tyr Arg Thr Ser Tyr Gln
 755 760 765
 Glu Glu Val Ile Lys Asn Ser Pro Val Lys Thr Phe Ala Ser Ala Thr
 770 775 780
 Phe Ser Ser Leu Leu Asp Val Phe Leu Ser Thr Thr Val Phe Leu Ile
 785 790 795 800
 Leu Ser Ile Thr Cys Phe Leu Lys Tyr Gly Ala Thr Ala Thr Pro Pro
 805 810 815
 Pro Pro Ala Ala Leu Ala Val Phe Gly Ala Asp Leu Leu Leu Glu Val
 820 825 830
 Leu Ser Leu Ile Val Ser Ile Arg Met Val Phe Phe Leu Glu Asp Val
 835 840 845
 Met Thr Cys Thr Lys Trp Leu Leu Glu Trp Ile Ala Gly Trp Leu Pro
 850 855 860
 Arg His Cys Ile Gly Ala Ile Leu Val Ser Leu Pro Ala Leu Ala Val
 865 870 875 880
 Tyr Ser His Ile Thr Ser Glu Phe Glu Thr Asn Ile His Val Thr Met
 885 890 895
 Phe Thr Gly Ser Ala Val Leu Val Ala Val Val His Tyr Cys Asn Phe
 900 905 910
 Cys Gln Leu Ser Ser Trp Met Arg Ser Ser Leu Ala Thr Ile Val Gly
 915 920 925
 Ala Gly Leu Leu Leu Leu Leu His Ile Ser Leu Cys Gln Asp Ser Ser
 930 935 940
 Ile Val Met Ser Pro Leu Asp Ser Ala Gln Asn Phe Ser Ala Gln Arg
 945 950 955 960
 Asn Pro Cys Asn Ser Ser Val Leu Gln Asp Gly Arg Arg Pro Ala Ser
 965 970 975
 Leu Ile Gly Lys Glu Leu Ile Leu Ile Phe Phe Leu Leu Leu Leu Leu
 980 985 990
 Val Trp Phe Leu Asn Arg Glu Phe Glu Val Ser Tyr Arg Leu His Tyr
 995 1000 1005
 His Gly Asp Val Glu Ala Asp Leu His Arg Thr Lys Ile Gln Ser Met
 1010 1015 1020

Arg Asp Gln Ala Asp Trp Leu Leu Arg Asn Ile Ile Pro Tyr His Val
 1025 1030 1035 1040
 Ala Glu Gln Leu Lys Val Ser Gln Thr Tyr Ser Lys Asn His Asp Ser
 1045 1050 1055
 Gly Gly Val Ile Phe Ala Ser Ile Val Asn Phe Ser Glu Phe Tyr Glu
 1060 1065 1070
 Glu Asn Tyr Glu Gly Gly Lys Glu Cys Tyr Arg Val Leu Asn Glu Leu
 1075 1080 1085
 Ile Gly Asp Phe Asp Glu Leu Leu Ser Lys Pro Asp Tyr Asn Ser Ile
 1090 1095 1100
 Glu Lys Ile Lys Thr Ile Gly Ala Thr Tyr Met Ala Ala Ser Gly Leu
 1105 1110 1115 1120
 Asn Thr Ala Gln Cys Gln Glu Gly Gly His Pro Gln Glu His Leu Arg
 1125 1130 1135
 Ile Leu Phe Glu Phe Ala Lys Glu Met Met Arg Val Val Asp Asp Phe
 1140 1145 1150
 Asn Asn Asn Met Leu Trp Phe Asn Phe Lys Leu Arg Val Gly Phe Asn
 1155 1160 1165
 His Gly Pro Leu Thr Ala Gly Val Ile Gly Thr Thr Lys Leu Leu Tyr
 1170 1175 1180
 Asp Ile Trp Gly Asp Thr Val Asn Ile Ala Ser Arg Met Asp Thr Thr
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 Gly Val Glu Cys Arg Ile Gln Val Ser Glu Glu Ser Tyr Arg Val Leu
 1205 1210 1215
 Ser Lys Met Gly Tyr Asp Phe Asp Tyr Arg Gly Thr Val Asn Val Lys
 1220 1225 1230
 Gly Lys Gly Gln Met Lys Thr Tyr Leu Tyr Pro Lys Cys Thr Asp Asn
 1235 1240 1245
 Gly Val Val Pro Gln His Gln Leu Ser Ile Ser Pro Asp Ile Arg Val
 1250 1255 1260
 Gln Val Asp Gly Ser Ile Gly Arg Ser Pro Thr Asp Glu Ile Ala Asn
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 Leu Val Pro Ser Val Gln Tyr Ser Asp Lys Ala Ser Leu Gly Ser Asp
 1285 1290 1295
 Asp Ser Thr Gln Ala Lys Glu Ala Arg Leu Ser Ser Lys Arg Ser Trp
 1300 1305 1310
 Arg Glu Pro Val Lys Ala Glu Glu Arg Phe Pro Phe Gly Lys Ala Ile
 1315 1320 1325

Glu Lys Asp Ser Cys Glu Asp Ile Gly Val Glu Glu Ala Ser Glu Leu
1330 1335 1340

Ser Lys Leu Asn Val Ser Lys Ser Val
1345 1350